



Brook Trout Genetics

Introduction

Historic stocking records indicate that 16 park streams were subjected to introductions of hatchery reared brook trout of the eastern strain by the Virginia Department of Game and Inland Fisheries during the late 1930s and the 1940s. During 1955, 13 park streams including seven from the previous group, were stocked with hatchery reared brook trout of the southern Appalachian strain by the U.S. Fish and Wildlife Service. As stream surveys were extended to small park streams during the late 1950s, a substantial number of the unmanaged streams were found to contain populations of what are thought to be native brook trout. Since 2001, brook trout populations in park streams have been included in a multi park evaluation of brook trout genetic relationships that is being conducted by the U.S. Geological Survey, Leetown Science Center.



Male brook trout.

Management Needs

The traditional method of addressing the decline of native trout populations has been hatchery supplementation. Introduction of hatchery stock leads to genetic modification. Of current brook trout populations within the northeastern United States, less than 5 % are reputed to consist of wild sources that have not been genetically modified by hatchery supplementation. However, nearly half of the brook trout populations within Shenandoah National Park are believed to consist of original wild populations.

Genetic diversity among populations is a requirement to ensure the species potential for adaptation to environmental changes. Effective conservation and restoration plans require clearly definable units of management. Contemporary molecular genetic techniques have proven to function as a robust conservation biology tool for identifying reproductive isolation among

populations, permitting the delineation of management units and allowing assessment of conservation priorities in existing populations. Thus, conservation and successful management of an exploited species requires baseline data on genetic diversity to ensure the maintenance of a sustainable native brook trout resource in the park.



Lower Big Run.

Current Procedures

Since 2001, approximately 2,400 brook trout from most of the known populations within the park have been sampled via adipose fin clips. At the time of collection, fin clips were individually stored in 95 % ethanol within small vials. Vials grouped by individual sites or by stream were then placed into cold storage prior to being shipped to the lab for DNA analysis.

Tissue from the fin clips was subjected to maximum likelihood assignment testing. Maximum likelihood assignment tests are qualitative assessments that partition the presence or absence of specific alleles, grouped gene sequences that comprise a genetic profile, within and between populations. Individual fish were genetically compared to fish from all other populations within the study and independently assigned back to a specific population based on allele characteristics. Allele characteristics in trout populations between streams and drainages differ to the extent that 98 % of all fish sampled were correctly assigned back to the original stream or site and 100% of all fish sampled were correctly assigned to their original drainage.

What We Have Learned

Statistical analyses have shown a high degree of genetic differentiation in trout among the three major park drainages and among tributaries within the drainages. Brook trout from the six Rappahannock River drainage samples that have been analyzed are highly divergent from



Brook Trout Genetics (continued...)

the fish sampled from the Shenandoah and James Rivers. A range- wide comparison of brook trout indicates that the fish inhabiting the upper reaches of the Rappahannock River are genetically similar to southern Appalachian brook trout sampled from Great Smoky Mountains. This result appears consistent with historical stocking records, yet contradicts the conclusion reached decades ago that the introductions of the non- native brook trout were unsuccessful. This study is currently funded through 2006.

References

Angers, B., L. Bernatchez, A. Angers, and L. Desgroseilliers. 1995. Specific microsatellite loci for brook charr reveal strong population subdivision on a microgeographic scale. *J. Fish Biol.* 47: 177- 185.

Ferguson, M.M. 1990. The genetic impact of introduced fishes on native species. *Can. J. Zool.* 68: 1053- 1057.

King, T.L., S.E. Julian, R. Coleman, R.P. Morgan II, M. Burnham- Curtis. In Preparation. Microsatellite DNA variation in brook trout (*Salvelinus fontinalis*) and cross- species amplification among related salmonids. To be submitted to *Molecular Ecology*. Kriegler, F.J., G.F. McCracken, J.W.

Habera, and R.J. Strange. 1995. Genetic characterization of Tennessee brook trout populations and associated management implications. *No. Amer. J. Fish. Manage.* 15:804- 813.

McCracken, G. F., C. R. Parker, and S. Z. Guffey. 1993. Genetic differentiation and hybridization between stocked hatchery and native brook trout in Great Smoky Mountains National Park. *Trans. Amer. Fish. Soc.* 122: 533- 542.

Stoneking, M., D.J. Wagner, and A.C. Hildebrand. 1981. Genetic evidence suggesting subspecific differences between northern and southern populations of brook trout (*Salvelinus fontinalis*). *Copeia* 1981:810- 819.



Virginia Commission of Game and Inland Fisheries stocking Ivy Creek with brook trout (Feb 1941).